



SEQUENCE LISTING

<110> Turck, Jutta
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<120> CONTROL OF GENE EXPRESSION IN EUKARYOTES

<130> 13101/48202

<140> US 10/732,859

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<170> PatentIn version 3.3

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Arg Asn Pro	Ser Ala Ala Glu Arg	Asp Ala Arg Glu Gln	Arg Val			
1600	1605	1610				
atc acc gcc	ggg cgg gac ttc gcc	gcc ggc acc gcc gcc	atc cag	6410		
Ile Thr Ala	Gly Arg Asp Phe Ala	Ala Gly Thr Ala Ala	Ile Gln			
1615	1620	1625				
cca ctg aac	ccc gaa tgg gac cgg	cac ctg ctc gac gtc	ctc gcc	6455		
Pro Leu Asn	Pro Glu Trp Asp Arg	His Leu Leu Asp Val	Leu Ala			
1630	1635	1640				
tcc ggc gac	ctc gag cag atc gac	gcg tgg acc aac gac	tgg ttc	6500		
Ser Gly Asp	Leu Glu Gln Ile Asp	Ala Trp Thr Asn Asp	Trp Phe			
1645	1650	1655				
gtc gaa cag	gcc gga cac tcc tcc	cac gaa gtg cgc acc	tgg atc	6545		
Val Glu Gln	Ala Gly His Ser Ser	His Glu Val Arg Thr	Trp Ile			
1660	1665	1670				
gcc gcg tac	gcg gca atg agc gcc	gcc ggg aag tac cgc	gtc acc	6590		
Ala Ala Tyr	Ala Ala Met Ser Ala	Ala Gly Lys Tyr Arg	Val Thr			
1675	1680	1685				
tcg acc ttc	tac cgc gaa atc cac	gag tgg ata gca gga	ttc ggg	6635		
Ser Thr Phe	Tyr Arg Glu Ile His	Glu Trp Ile Ala Gly	Phe Gly			
1690	1695	1700				
att act acc	gcc gtc gcc gtc gac	gaa tag accccgccgc	tcccgccccg	6685		
Ile Thr Thr	Ala Val Ala Val Asp	Glu				
1705	1710					
cagtcccaac	gaaggggtggc	cccggatgac	ctccgtccgc	ccgtgctcgc	cgtcgggtgaa	6745
cgcgggctgg	tcgggtgggca	ggaagacctc	atcgccgaca	tcgccctoga	cctcgcagct	6805
cgtcagtagg	aatgcgcacg	ggccgacgag	tcgcgctggt	caccggggcc	agccgcggca	6865
tcggggcggc	catcgcagat	gcggtggccg	cctccggtgc	cgccgtaatc	gtccactacg	6925
gatccgatcg	gacggccgcc	gctgcggtgt	cgacggcatc	acggctgccg	ggggcctcgc	6985
ggctgcggtc	caggccgacc	tgtccccgacc	cgaggggcct	gaagagctga	tgccgggagtt	7045
cgactccgcg	ctcgacggtc	tcgggctoga	ccgagggctc	gacatcctcg	tcaacaacgc	7105
cggaatcagt	cggcgcggag	cgctcgagcg	cgtcactgtc	gaggatttcg	accgtctggt	7165

cgcactcaac cagcgcgccc cggttcttctg gactcggcat gccctgcccc ggatgcacga 7225
 cggcggtcgc atcgtcaaca tttcctccgg atccgccccg tacgccagac ccgacgtcat 7285
 cagctacgcc atgaccaagg gggcgatcga ggtgctcacc cgcgccctcg ccgtagacgt 7345
 cggcgaacga ggcatacccg ccaacgcctg ggcgcgggcc gcgctcgata ccgacatgaa 7405
 cgcgcactgg cttcgcggtg acgaccatgc ccgcaccacc gccgcgtcca ccaactgcact 7465
 gcgaaaactc gccaccgcgg aggcacatgc cgcgatcgtg gccttctctg tcagcgcgcg 7525
 cgccggtgcg atcaccgggc aggtcatcga cgccaccaac ggcaaccggc tctaaccaga 7585
 attaccggg tccc 7599

<210> 2
 <211> 246
 <212> PRT
 <213> Rhodococcus sp.
 <400> 2

Met	Thr	Thr	Thr	Asp	Thr	Gly	Pro	Lys	Pro	Gly	Ser	Glu	Ala	Ala	Ala	1	5	10	15
Leu	Leu	Ala	Asn	Val	Arg	Thr	Ser	Gly	Ala	Arg	Leu	Ser	Ser	Ala	Leu	20	25	30	
Tyr	Asp	Ile	Leu	Lys	Asn	Arg	Leu	Leu	Glu	Gly	Arg	Tyr	Ala	Ala	Gly	35	40	45	
Glu	Lys	Ile	Val	Val	Glu	Ser	Ile	Arg	Gln	Glu	Phe	Gly	Val	Ser	Lys	50	55	60	
Gln	Pro	Val	Met	Asp	Ala	Leu	Arg	Arg	Leu	Ser	Ser	Asp	Lys	Leu	Val	65	70	75	80
His	Ile	Val	Pro	Gln	Val	Gly	Cys	Glu	Val	Val	Ser	Tyr	Ala	Pro	Arg	85	90	95	
Glu	Val	Glu	Asp	Phe	Tyr	Thr	Leu	Phe	Gly	Gly	Phe	Glu	Gly	Thr	Ile	100	105	110	
Ala	Ala	Val	Ala	Ala	Ser	Arg	Arg	Thr	Glu	Ala	Gln	Leu	Leu	Glu	Leu	115	120	125	

Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro
130 135 140

Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala
145 150 155 160

Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln
165 170 175

Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr
180 185 190

Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu
195 200 205

Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala
210 215 220

Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser
225 230 235 240

Asn Ala Gln Leu Pro Ser
245

<210> 3
<211> 514
<212> PRT
<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser Pro
1 5 10 15

Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu Arg
20 25 30

Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val Ser
35 40 45

Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala Met
50 55 60

Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile Tyr
65 70 75 80

Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp Val
 85 90 95

Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val Gly
 100 105 110

Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly Asp
 115 120 125

Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met Gly
 130 135 140

Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile Gly
 145 150 155 160

Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly Phe
 165 170 175

Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu His
 180 185 190

Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met Gly
 195 200 205

Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val Ser
 210 215 220

Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro Phe
 225 230 235 240

Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu Ser
 245 250 255

Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala Val
 260 265 270

Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu Ile
 275 280 285

Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr Ile
 290 295 300

Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile Ser
305 310 315 320

Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala Val
325 330 335

Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg Lys
340 345 350

Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala Pro
355 360 365

Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala Ala
370 375 380

Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val Thr
385 390 395 400

Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser Gly
405 410 415

Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe Ala
420 425 430

Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn Ser
435 440 445

Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser Val
450 455 460

Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln Leu
465 470 475 480

Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu Thr
485 490 495

Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val Leu
500 505 510

Asp Lys

<210> 4
 <211> 637
 <212> PRT
 <213> Rhodococcus sp.

<400> 4

Val Met Thr Asp Met Ser Asp His Asp Arg Thr Ser Tyr Asp Thr Asp
 1 5 10 15

Val Val Ile Val Gly Leu Gly Pro Ala Gly Gly Thr Ala Ala Leu Ala
 20 25 30

Leu Ala Ser Tyr Gly Ile Arg Val His Ala Val Ser Met Phe Pro Trp
 35 40 45

Val Ala Asn Ser Pro Arg Ala His Ile Thr Asn Gln Arg Ala Val Glu
 50 55 60

Val Leu Arg Asp Leu Gly Val Glu Asp Glu Ala Arg Asn Tyr Ala Thr
 65 70 75 80

Pro Trp Asp Gln Met Gly Asp Thr Leu Phe Thr Thr Ser Leu Ala Gly
 85 90 95

Glu Glu Ile Val Arg Met Gln Thr Trp Gly Thr Gly Asp Ile Arg Tyr
 100 105 110

Gly Asp Tyr Leu Ser Gly Ser Pro Cys Thr Met Leu Asp Ile Pro Gln
 115 120 125

Pro Leu Met Glu Pro Val Leu Ile Lys Asn Ala Ala Glu Arg Gly Ala
 130 135 140

Val Ile Ser Phe Asn Thr Glu Tyr Leu Asp His Ala Gln Asp Glu Asp
 145 150 155 160

Gly Val Thr Val Arg Phe Arg Asp Val Arg Ser Gly Thr Val Phe Thr
 165 170 175

Gln Arg Ala Arg Phe Leu Leu Gly Phe Asp Gly Ala Arg Ser Lys Ile
 180 185 190

Ala Glu Gln Ile Gly Leu Pro Phe Glu Gly Glu Leu Ala Arg Ala Gly
 195 200 205

Thr Ala Tyr Ile Leu Phe Asn Ala Asp Leu Ser Lys Tyr Val Ala His
 210 215 220

Arg Pro Ser Ile Leu His Trp Ile Val Asn Ser Lys Ala Gly Phe Gly
 225 230 235 240

Glu Ile Gly Met Gly Leu Leu Arg Ala Ile Arg Pro Trp Asp Gln Trp
 245 250 255

Ile Ala Gly Trp Gly Phe Asp Met Ala Asn Gly Glu Pro Asp Val Ser
 260 265 270

Asp Asp Val Val Leu Glu Gln Ile Arg Thr Leu Val Gly Asp Pro His
 275 280 285

Leu Asp Val Glu Ile Val Ser Arg Ser Phe Trp Tyr Val Asn Arg Gln
 290 295 300

Trp Ala Glu His Tyr Gln Ser Gly Arg Val Phe Cys Gly Gly Asp Ala
 305 310 315 320

Val His Arg His Pro Pro Ser Ser Gly Leu Gly Ser Asn Thr Ser Met
 325 330 335

Gln Asp Ala Phe Asn Leu Ala Trp Lys Ile Ala Phe Val Val Lys Gly
 340 345 350

Tyr Ala Gly Pro Gly Leu Leu Glu Ser Tyr Ser Pro Glu Arg Val Pro
 355 360 365

Val Gly Lys Gln Ile Val Ala Arg Ala Asn Gln Ser Arg Lys Asp Tyr
 370 375 380

Ala Gly Leu Arg Glu Trp Phe Asp His Glu Ser Asp Asp Pro Val Ala
 385 390 395 400

Ala Gly Leu Ala Lys Leu Lys Glu Pro Ser Ser Glu Gly Val Ala Leu
 405 410 415

Arg Glu Arg Leu Tyr Glu Ala Leu Glu Val Lys Asn Ala Glu Phe Asn
 420 425 430

Ala Gln Gly Val Glu Leu Asn Gln Arg Tyr Thr Ser Ser Ala Val Val
 435 440 445

Pro Asp Pro Glu Ala Gly Glu Glu Val Trp Val Arg Asp Arg Glu Leu
 450 455 460

Tyr Leu Gln Ala Thr Thr Arg Pro Gly Ala Lys Leu Pro His Ala Trp
 465 470 475 480

Leu Val Gly Ala Asp Gly Thr Arg Ile Ser Thr Leu Asp Val Thr Gly
 485 490 495

Lys Gly Met Met Thr Leu Leu Thr Gly Leu Gly Gly Gln Ala Trp Lys
 500 505 510

Arg Ala Ala Ala Lys Leu Asp Leu Pro Phe Leu Arg Thr Val Val Val
 515 520 525

Gly Glu Pro Gly Thr Ile Asp Pro Tyr Gly Tyr Trp Arg Arg Val Arg
 530 535 540

Asp Ile Asp Glu Ala Gly Ala Leu Leu Val Arg Pro Asp Gly Tyr Val
 545 550 555 560

Ala Trp Arg His Ser Ala Pro Val Trp Asp Asp Thr Glu Ala Leu Thr
 565 570 575

Ser Leu Glu Asn Ala Leu Thr Ala Val Leu Asp His Ser Ala Ser Asp
 580 585 590

Asn Gly Asn Pro Ser Gly Thr Asn Glu Pro Gln Tyr Ser Thr Arg Ala
 595 600 605

Val Pro Ile Val Val Pro His Val Thr Ala Glu Asp Ala Ala Pro Ala
 610 615 620

Ser Ala Thr Arg Thr Thr Thr Val Glu Gly Glu Asn Arg
 625 630 635

<210> 5
 <211> 314
 <212> PRT
 <213> Rhodococcus sp.

<400> 5

Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly Arg
 1 5 10 15

Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe Asp
 20 25 30

His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val Ile
 35 40 45

Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro Pro
 50 55 60

Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr Glu
 65 70 75 80

Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala Arg
 85 90 95

Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met His
 100 105 110

Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser Ile
 115 120 125

Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu Pro
 130 135 140

Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly Arg
 145 150 155 160

Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly Gly
 165 170 175

Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu Glu
 180 185 190

Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu Arg
 195 200 205

Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala Ala
 210 215 220

Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His Leu
 225 230 235 240

Leu Asp Val Leu Ala Ser Gly Asp Leu Glu Gln Ile Asp Ala Trp Thr
 245 250 255

Asn Asp Trp Phe Val Glu Gln Ala Gly His Ser Ser His Glu Val Arg
 260 265 270

Thr Trp Ile Ala Ala Tyr Ala Ala Met Ser Ala Ala Gly Lys Tyr Arg
 275 280 285

Val Thr Ser Thr Phe Tyr Arg Glu Ile His Glu Trp Ile Ala Gly Phe
 290 295 300

Gly Ile Thr Thr Ala Val Ala Val Asp Glu
 305 310

<210> 6
 <211> 289
 <212> PRT
 <213> Rhodococcus sp.

<400> 6

Met Thr Arg Pro Tyr Thr Ser Val Trp Asp Asp Leu Asn Gln Val Glu
 1 5 10 15

Phe Ser Gln Gly Phe Ile Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu
 20 25 30

His Ala Gly Asp Ser Ser Lys Pro Thr Leu Ile Leu Leu His Gly Ile
 35 40 45

Thr Gly His Ala Glu Ala Tyr Val Arg Asn Leu Arg Ser His Ser Glu
 50 55 60

His Phe Asn Val Trp Ala Ile Asp Phe Ile Gly His Gly Tyr Ser Thr
 65 70 75 80

Lys Pro Asp His Pro Leu Glu Ile Lys His Tyr Ile Asp His Val Leu
85 90 95

Gln Leu Leu Asp Ala Ile Gly Val Glu Lys Ala Ser Phe Ser Gly Glu
100 105 110

Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu
115 120 125

Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn
130 135 140

Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys
145 150 155 160

Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala
165 170 175

Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile
180 185 190

Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu
195 200 205

Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu
210 215 220

Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro
225 230 235 240

Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly
245 250 255

Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu
260 265 270

Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg
275 280 285

Ser

<210>
<211>
<212>
<213>

<400> 7

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<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> OHPR3

<400> 8
atcgaattcg gatccatgac caccacc

27

<210> 9
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> OHPR4

<400> 9
atcgcgggccg ctctagacta actgcagggc gccaaagctcg gcag

44

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> C11

<400> 10
atcgaattcg gatccacgag agag

24

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> C12

<400> 11
atccggccgc gctctagagt acgcaagct

29

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> op1

<400> 12
atcctcgaga ccccgatacc

20

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> op2

<400> 13
atcgtcgacc gctaccc

17

<210> 14
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop2

<400> 14
tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc

50

<210> 15
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop3

<400> 15
atgctagacg tctagttcag acgctactta tatagaggaa gggctcttgcg

50

<210> 16
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> CaMVop4

<400> 16		
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<210> 17		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> CaMVopF1		
<400> 17		
atcgatatct ccactgacgt aag		23
<210> 18		
<211> 24		
<212> DNA		
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<220>		
<223> CaMVopR1		
<400> 18		
gatggatccg tcctctccaa atga		24
<210> 19		
<211> 470		
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<213> Artificial Sequence		
<220>		
<223> Chimeric promoter		
<400> 19		
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atacagtctc agaagaccag agggctattg agacttttca acaaagggtg atatcgggaa	120	
acctcctcgg attccattgc ccagctatct gtcacttcat cgaaaggaca gtagaaaagg	180	
aagatggctt ctacaaatgc catcattgcg ataaaggaaa ggctatcggt caagaatgcc	240	
tctaccgaca gtggtcccaa agatgtaccc ccacccacga ggaacatcgt ggaaaaagaa	300	
gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg	360	
gatgacgcac aatcccacta tccttcgcaa gacccttctt ctatataagt agcgtctgaa	420	
ctagacgtct agcattctag ttgaggaagt tcatttcatt tggagaggac	470	